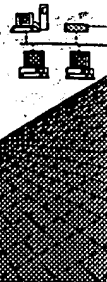D. Wortman

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/147,801A_

Art Unit / Team No. : _1645_

Date Processed by STIC: _5/11/2000_

TC 1600 MAIL ROOM   MAY 23 2000   RECEIVED

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION   SERIAL NUMBER: _09/147,801A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                                This may occur if your file was retrieved in a word processor after creating it.
                                Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
                                This may occur if your file was retrieved in a word processor after creating it.
                                Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
         Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                As per the rules, each n or Xaa can only represent a single residue.
                                Please present the maximum number of each residue having variable length and
                                indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                to the subsequent amino acid sequence.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
         (OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
                                (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                This sequence is intentionally skipped

                                Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
         (NEW RULES)   **<210> sequence id number**
                                <400> sequence id number
                                000

10 _____ Use of **n's** or **Xaa's**   Use of n's and/or Xaa's have been detected in the Sequence Listing.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response.
         (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
         (NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                Please explain source of genetic material in <220> to <223> section.
                                (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                                file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                Instead, please use "File Manager" or any other means to copy file to floppy disk.

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other:

Applicant Must Provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
Technical Assistance......................................703-287-0200
To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

D. Wortman

```
        RAW SEQUENCE LISTING              DATE: 05/11/2000
        PATENT APPLICATION:  US/09/147,801A     TIME: 16:08:10
```

Does Not Comply
Corrected Diskette Needed

```
        Input Set : A:\PICORNA1.txt
        Output Set: N:\CRF3\05112000\I147801A.raw
```

```
       3 <110> APPLICANT: NIKLASSON, Bo
       5 <120> TITLE OF INVENTION: NEW PICORNA VIRUSES, VACCINES AND DIAGNOSTIC KITS
       7 <130> FILE REFERENCE: REF/Niklasson/801
       9 <140> CURRENT APPLICATION NUMBER: 09/147,801A
C--> 10 <141> CURRENT FILING DATE: 1999-03-11
      12 <150> PRIOR APPLICATION NUMBER: PCT/SE97/01515
      13 <151> PRIOR FILING DATE: 1997-09-09
      15 <160> NUMBER OF SEQ ID NOS: 4
      17 <170> SOFTWARE: PatentIn Ver. 2.1
      19 <210> SEQ ID NO: 1
      20 <211> LENGTH: 264
      21 <212> TYPE: DNA
      22 <213> ORGANISM: Picornaviridae
      24 <400> SEQUENCE: 1
      25 agtctagtct tatcttgtat gtgtcctgca ctgaacttgt ttctgtctct ggagtgctct 60
      26 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacaggtgg 120
      27 ctttcacctc tggacagtgc attccacacc cgctccacgg tagaagatga tgtgtgtctt 180
      28 tgcttgtgaa aagcttgtga aaatcgtgtg taggcgtagc ggctacttga gtgccagcgg 240
      29 attacccca gtggtaacac tagc                                     264
      32 <210> SEQ ID NO: 2
      33 <211> LENGTH: 264
      34 <212> TYPE: DNA
      35 <213> ORGANISM: Picornaviridae
      37 <400> SEQUENCE: 2
      38 agtctagttt cattctgtgt gtgtttggca ctgaaattat ttctgtctgt ggggtgcttt 60
W--> 39 acacttcagt aggggctgta cccgggcggt cccactcttc acaggaatc gcacaggtgg 120
      40 ctttcacctc tggacagtgc attccacacc cgctccacag tagaagatga tgtgtgtctt 180
W--> 41 tgcttgtgaa aagcttgtga aaatcgtgtg taggcgtagc ggtacttga gtgccagcgg 240
W--> 42 acaccccta gtggtaacac tagc                                     264
      45 <210> SEQ ID NO: 3
      46 <211> LENGTH: 264
      47 <212> TYPE: DNA
      48 <213> ORGANISM: Picornaviridae
      50 <400> SEQUENCE: 3
      51 agtttggttc tctcttgagt gtgttttgtg ttagcataat ttctgtctct agagtgcttt 60
      52 acactctagt aggggctgta cccgggcggt cccactcttc acaggaatct gcacaggtgg 120
      53 ctttcacctc tggacagtgc attccatacc cgctccacaa tagaagatga tgtatatctt 180
      54 tgtttgtgaa atgctcatga aacgtgtgtg taggcgtagc ggctacttga atgccagcgg 240
      55 aacccccta gtggtaacac tagc                                     264
      58 <210> SEQ ID NO: 4
      59 <211> LENGTH: 179
      60 <212> TYPE: PRT
      61 <213> ORGANISM: Picornaviridae
      63 <400> SEQUENCE: 4
      64 Lys Asp Leu Met Glu Ile Ala Arg Met Pro Ser Val Tyr Lys Gly Glu
      65  1               5                  10                  15
      67 Arg Thr Glu Pro Gly Gly Thr Asn Gly Tyr Phe Gln Trp Ser His Thr
```

see item 10 on Erra Summary Sheet

RAW SEQUENCE LISTING   DATE: 05/11/2000
PATENT APPLICATION: US/09/147,801A   TIME: 16:08:10

Input Set : A:\PICORNA1.txt
Output Set: N:\CRF3\05112000\I147801A.raw

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68              20                    25                    30
70 His Ser Pro Ile Asn Trp Val Phe Asp Gly Gly Ile His Leu Glu Asp
71          35                    40                    45
73 Met Pro Asn Leu Asn Leu Phe Ser Ser Cys Tyr Asn Tyr Trp Arg Gly
74      50                    55                    60
76 Ser Thr Val Leu Lys Leu Thr Val Tyr Ala Ser Thr Phe Asn Lys Gly
77 65                    70                    75                80
79 Arg Leu Arg Met Ala Phe Phe Pro Ile Met Met Gln Gly Thr Gln Arg
80              85                    90                    95
82 Lys Lys His Lys Cys Leu Phe Met Val Cys Asp Ile Gly Leu Asn Asn
83          100                   105                   110
85 Thr Phe Glu Met Thr Ile Pro Tyr Thr Trp Gly Asn Trp Met Arg Pro
86      115                   120                   125
88 Thr Arg Gly Ser Val Ile Gly Trp Leu Arg Ile Asp Val Leu Asn Arg
89      130                   135                   140
91 Leu Thr Tyr Asn Ser Ser Ser Pro Asn Ala Val Asn Cys Ile Leu Gln
92 145                   150                   155                160
94 Val Lys Met Gly Asn Asp Ala Lys Phe Met Val Pro Thr Thr Ser Asn
95              165                   170                   175
97 Ile Val Trp
```

VERIFICATION SUMMARY   DATE: 05/11/2000
PATENT APPLICATION: US/09/147,801A   TIME: 16:08:11

Input Set : A:\PICORNA1.txt
Output Set: N:\CRF3\05112000\I147801A.raw

```
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:39 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:39 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:39 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:39 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:41 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:41 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:41 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:41 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:42 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:42 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:42 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:42 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
```